





Db 53 PK-1VACA 59

## RESULT 4

US-09-925-409-1538

Sequence 1538: Application US/06045300

Patent No. US20020161681A1

GENERAL INFORMATION:

APPLICANT: Craig Rosen,

APPLICANT: Craig Rosen,

TITLE OF INVENTION: Molecule A-113, Proteases and Antibodies

FILE REFERENCE: PA101

CURRENT AFFILIATION NUMBER: US 09/925 300

CURRENT FILING DATE: 2001-08-10

PRIORITY APPLICATION NUMBER: PCT/US80/05988

PRIORITY FILING DATE: 2000-03-08

PRIORITY APPLICATION NUMBER: PCT/US80/05988

PRIORITY FILING DATE: 2000-03-08

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PRIORITY FILING DATE: 2000-03-08

PRIORITY APPLICATION NUMBER: PCT/US80/05988

INVENTION NUMBER: 12,783

REFERENCE: 1,324, 3, 11, 17, 010601

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 668 amino acids

TYPE: amino acid

ORGANISM: Homo sapiens

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-761-569-13

Query Match

Best Local Similarity: 24.3%; Pred. No. 3.9;

Matches: 24; Conservative: 21; Mismatches: 61; Indels: 18; Gaps: 59

Db 488 PK-1VACA 59

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Best Local Similarity: 24.3%; Pred. No. 3.9;

Matches: 24; Conservative: 21; Mismatches: 61; Indels: 18; Gaps: 59

Db 488 PK-1VACA 59

Query Match

Best Local Similarity: 24.3%; Pred. No. 3.9;

Matches: 24; Conservative: 21; Mismatches: 61; Indels: 18; Gaps: 59

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Matches: 24; Conservative: 21; Mismatches: 61; Indels: 18; Gaps: 59

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Matches: 24; Conservative: 21; Mismatches: 61; Indels: 18; Gaps: 59

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Matches: 24; Conservative: 21; Mismatches: 61; Indels: 18; Gaps: 59

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Matches: 24; Conservative: 21; Mismatches: 61; Indels: 18; Gaps: 59

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Matches: 24; Conservative: 21; Mismatches: 61; Indels: 18; Gaps: 59

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Matches: 24; Conservative: 21; Mismatches: 61; Indels: 18; Gaps: 59

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Matches: 24; Conservative: 21; Mismatches: 61; Indels: 18; Gaps: 59

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Matches: 24; Conservative: 21; Mismatches: 61; Indels: 18; Gaps: 59

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Best Local Similarity: 24.3%; Pred. No. 3.9;

Matches: 24; Conservative: 21; Mismatches: 61; Indels: 18; Gaps: 59

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Best Local Similarity: 24.3%; Pred. No. 3.9;

Matches: 24; Conservative: 21; Mismatches: 61; Indels: 18; Gaps: 59

Db 488 PK-1VACA 59



PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US98/06677

STUD. NO. 128  
LENGTH: 491



Tue Nov 12 16:06:51 2002

us-09-899-917-2.rapp

Page 7

Search completed: November 12, 2002, 09:26:49  
Jed's time : 12 Steps









14 158 TIMCS 162

# RESULT 1

AAV84000

14 AAV84000 standard; Protein: 162 AA.

AC AAV84000;

25-OCT-2000 (first entry)

Human B-cell surface protein MD-1.

Human B cell surface protein; apoptosis; anti-allergic; allergy; ESI; anti-asthmatic; immunosuppressive; dermatological; anti-inflammatory; autoimmune diseases; asthma; atopic dermatitis; expressed sequence tag.

Human sapiens.

Key: Location/Qualifiers

Peptide 1-19

Protein 20-162

Note: "mature MD-1 protein"

JP2000106880-A.

18-APR-2000.

08-OCT-1999; 98JP-0296470.

08-OCT-1999; 98JP-0296470.

08-OCT-1999; 98JP-0296470.

08-OCT-1999; 98JP-0296470.

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08-OCT-1999; 98JP-0296470.

08-OCT-1999; 98JP-0296470.

14-JUL-1999 (first entry)

Mouse OHP106 protein.

CHP106, bacterial virus; infectious; cytokine activity; tissue formation; cell proliferation; cell differentiation; immunostimulation; therapy; immunosuppression; hematopoiesis control; tissue repair.

Mus musculus.

W09918205-A1.

15-APR-1999.

06-OCT-1998; 98WO-JP04515.

07-OCT-1997; 97JP-0274674.

(ONV) CHN PHARM CO LTD.

Honjo I, Kato K, Tada H;

WPI; 1999-277259/23.

NIGLS; AAX06603, AAX06694.

New polypeptides useful in the treatment of various diseases including bacterial and viral infections with cytokine activity

Claim 1; Page 44; 57pp; Japanese.

This sequence represents a CHP106 protein of the invention.

The polypeptides and their analogs are applicable in drug compositions useful for treatment of various diseases including bacterial and viral infections with cytokine activity and activities

e.g. on cell proliferation/differentiation, immunostimulation/suppression, control of haematopoiesis, and tissue formation and repair. The proteins and peptides have a wide spectrum of activities.

Sequence 162 AA;

Query Match

Best Local Similarity 14.2% Score 73; DB 21; Length 162;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

107 KPSFQDRKKGQIYVAPVNN 129

107 KPSFQDRKKGQIYVAPVNN 129

107 KPSFQDRKKGQIYVAPVNN 129

107 KPSFQDRKKGQIYVAPVNN 129

107 KPSFQDRKKGQIYVAPVNN 129

107 KPSFQDRKKGQIYVAPVNN 129

107 KPSFQDRKKGQIYVAPVNN 129

107 KPSFQDRKKGQIYVAPVNN 129

107 KPSFQDRKKGQIYVAPVNN 129

107 KPSFQDRKKGQIYVAPVNN 129

107 KPSFQDRKKGQIYVAPVNN 129

107 KPSFQDRKKGQIYVAPVNN 129

107 KPSFQDRKKGQIYVAPVNN 129

107 KPSFQDRKKGQIYVAPVNN 129

107 KPSFQDRKKGQIYVAPVNN 129



Copyright (c) 1994 - 2002 Computer 130.

MM Project: Project search, using sw model

Run on: November 12, 2002, 09:26:56 / Search time 17 seconds

(without alignments) 916,104 Million cell updates/sec

Hit: US-09-899-917-2

Project score: 162

Sequence: 1 MPEPTALEWETTFEPTL.....EYTHKESVAZAMTTRIS 172

Search length: 1100

Word size: 10

Total number of hits satisfied chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 1000 summaries

Database: PK\_73:  
1: PK1:  
2: PK2:  
3: PK3:  
4: PK4:

Prod. No. is the number of results predicted by change to have a score greater than or equal to the score of the result being produced, and is derived by analysis of the total score distribution.

#### SUMMARIES

Prod. No.	Score	Match	Length	DB	Description
No matches found					

Search completed: November 12, 2002, 09:29:12  
Run time: 17 secs



GeneDoc version 5.1.4  
Copyright (c) 1998 - 2002. Computer Ltd.

FASTA Protein: Protein search, using SW model

Run on: November 12, 2002, 09:23:55, Search time 1.2 seconds

(without alignment)  
559,960 Million cell updates/sec

Title:

US-09-899-917-2

Perfect score: 162

Sequence:

1 M02TALPFWLHPLHSNSR.....ELTKRSIVAVNALLMS 162

Search table:

all 30

Search:

112892 seqs, 4147628 residues

Word size:

10

Total number of hits satisfying chosen parameters: 2

Maximum hit seq length:

20000000

Maximum hit seq length: 20000000

Post-processing: listing first 1000 similarities

Database: SwissProt 401\*

Prod. No. is the number of protein's production by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARY

Result	No.	Score	Match	Length	DB	ID	Accession
1	162	139.0	162	1	M01_HUMAN	004711	human sapient
2	23	14.2	162	1	M01_MOUSE	004711	mouse musculus

#### ALIGNMENTS

RESULT 1  
M01\_HUMAN STANDARD, P04: 162 AA.

AC 15-JUN-2002 (rel. 41, created)

BT 15-JUN-2002 (rel. 41, last sequence update)

DE 15-JUN-2002 (rel. 41, last annotation update)

HE M01 protein precursor.

IN M01.

CS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OX Mammalia; Eutheria; Primates; Catartida; Hominidae; Homo;

XX M01-taxid-9606;

EN 11

SEQUENCE FROM N.A.

RE 15-JUN-2002 (rel. 41, created)

BT 15-JUN-2002 (rel. 41, last sequence update)

DE 15-JUN-2002 (rel. 41, last annotation update)

HE M01 protein precursor (lymphocyte antigen 86)

IN M01.

CS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;

XX M01-taxid-10090;

EN 11

SEQUENCE FROM N.A. AND SEQUENCE OF 20-44.

RA 15-JUN-2002 (rel. 41, created)

BT 15-JUN-2002 (rel. 41, last sequence update)

DE 15-JUN-2002 (rel. 41, last annotation update)

HE M01 protein precursor (lymphocyte antigen 86)

IN M01.

CS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;

XX M01-taxid-10090;

EN 11

SEQUENCE FROM N.A. AND SEQUENCE OF 20-44.

RA 15-JUN-2002 (rel. 41, created)

BT 15-JUN-2002 (rel. 41, last sequence update)

DE 15-JUN-2002 (rel. 41, last annotation update)

HE M01 protein precursor (lymphocyte antigen 86)

IN M01.

CS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;

XX M01-taxid-10090;

EN 11

SEQUENCE FROM N.A. AND SEQUENCE OF 20-44.

RA 15-JUN-2002 (rel. 41, created)

BT 15-JUN-2002 (rel. 41, last sequence update)

DE 15-JUN-2002 (rel. 41, last annotation update)

HE M01 protein precursor (lymphocyte antigen 86)

IN M01.

CS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;

XX M01-taxid-10090;

EN 11

SEQUENCE FROM N.A. AND SEQUENCE OF 20-44.

RA 15-JUN-2002 (rel. 41, created)

BT 15-JUN-2002 (rel. 41, last sequence update)

DE 15-JUN-2002 (rel. 41, last annotation update)

HE M01 protein precursor (lymphocyte antigen 86)

IN M01.

CS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;

XX M01-taxid-10090;

EN 11

SEQUENCE FROM N.A. AND SEQUENCE OF 20-44.

RE TISSUE RECOIL:  
 RA REFLINE 98449466; PubMed 9686507;  
 RA Miyake K., Shimazu Y., Kondo J., Niki T., Akashi S., Ogata H.,  
 RA Yamashita Y., Mura Y., Kimoto M.,  
 RA "mouse MD-1, a molecule that is physically associated with CD105 and  
 RA positively regulates its expression."  
 RA Immunol. 161:1448-1453(1998).  
 RA 121  
 RA TISSUE RECOIL:  
 RA REFLINE 20384784; PubMed 10925274;  
 RA Goleczyński R.M., Chen Z., Clark D.A., Hu J., Yu G., Li X., Tsang W.,  
 RA Hudali S.,  
 RA "regulation of gene expression of murine MD-1 regulates subsequent T  
 RA cell activation and cytokine production."  
 RA Immunol. 165:1925-1932(2000).  
 RA 122  
 RA TISSUE RECOIL: May cooperate with CD180 and TLR4 to mediate the innate  
 RA immune response to bacterial lipopolysaccharide (LPS) and cytokine  
 RA production. Important for efficient CD180 cell surface expression.  
 RA 123  
 RA SUBUNIT: Binds CD180.  
 RA 124  
 RA SUBCELLULAR LOCATION: Extracellular; associated with CD180 at the  
 RA cell surface.  
 RA 125  
 RA TISSUE SPECIFICITY: Highly expressed in spleen, liver, brain and  
 RA thymus, and at lower levels in kidney.  
 RA 126  
 RA SIMILARITY: BELONGS TO THE MD FAMILY.  
 RA 127  
 RA 128  
 RA This SWISS-PROT entry is copyright. It is produced through a collaboration  
 RA between the European Bioinformatics Institute. There are no restrictions on its  
 RA use by non-profit institutions as long as its content is in no way  
 RA modified and this statement is not removed, used by and for commercial  
 RA entities requires a license agreement (see <http://www.ebi.ac.uk/submit>  
 RA or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 RA 129  
 RA EMBL: AB007599; BAA32399.1;  
 RA 130  
 RA MIM: 6011421404; 1986.  
 RA 131  
 RA Immune response; inflammatory response; Signal.  
 RA 132  
 RA KW SIGNAL.  
 RA 133  
 RA CHAIN 20 162 MD-1 PROTEIN.  
 RA 134  
 RA CATHID 96 96 R: UNK (GILVNA) (POTENTIAL).  
 RA 135  
 RA CATHID 156 156 N-LINKED (GILVNA) (POTENTIAL).  
 RA 136  
 RA CATHID 1781 1781 MW: EED2DEDA64A9472F; c18c64;  
 RA 137  
 RA SEQUENCE 162 AA; 1781 MW; EED2DEDA64A9472F; c18c64;  
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==== Protein Match search, using SW model

Run on: November 12, 2002, 09:26:26 : Search time 41 seconds

(without alignment)

1076,762 Million cell operators/sec

File: US-09-899-917-2

Protein source

Sequence: 1 MESTAT1P[EMBL]11959581.....ELECTROLYTIC CHANNELS [P.2

Search filter

filter: -drop 60.0 -dropw 60.0

Search: 671540 seqs, 20047115 residues

Word size: 10

Total number of hits satisfying chosen parameters: 0

Minimum for seq length: 0

Maximum for seq length: 2000000000

Post-processing: listing first 1000 summaries

Database: SLKREMBL\_21:

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_humani:\*
- 5: sp\_invertebrates:\*
- 6: sp\_mammali:\*
- 7: sp\_meli:\*
- 8: sp\_ornithelli:\*
- 9: sp\_planci:\*
- 10: sp\_planti:\*
- 11: sp\_rodenti:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrati:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriophage:\*
- 17: sp\_archaea:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result found printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Prod. No.	Score	Match Length (B)	Prod. No.
No matches found			

Search completed: November 12, 2002, 09:28:27  
Job time: 41 secs





























[illegible]











[illegible]



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2  11S:  (08-540-950-) 3

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[illegible]





















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01 phosphate (gamma-UTP) + L-glutamate  
02 SUBUNIT: heterodimer of A, B and C subunits (by similarity)  
03 CATALYTIC: subunit 1 (the catalytic subunit)  
04  
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12 Locus: A0013029, AAM24877.1  
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QUALITY MATCHES	24/08	SCORE	77	108	2	LENGTH	7:59
POST-FOOT STIMULI	24/08	PROD NO.	13				
MATCHES	25/	CONSERVATIVE	17	MISMATCHES	40	INDICES	42
							CHAPS
02	42	144	144	144	144	144	144
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04	10	10	10	10	10	10	10
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05	27	44	44	44	44	44	44
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	1	1	1	1	1	1	1

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